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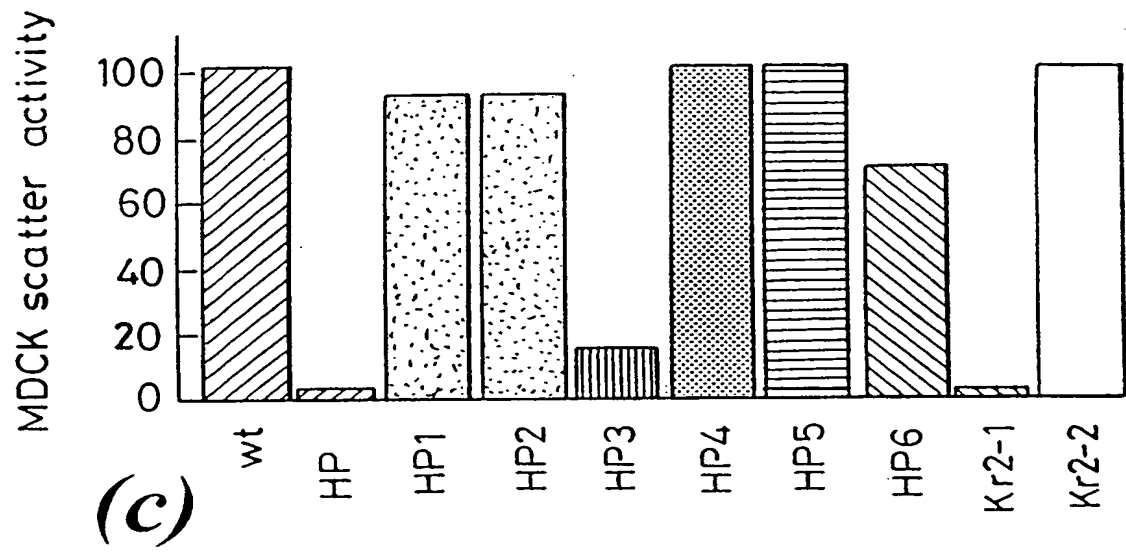
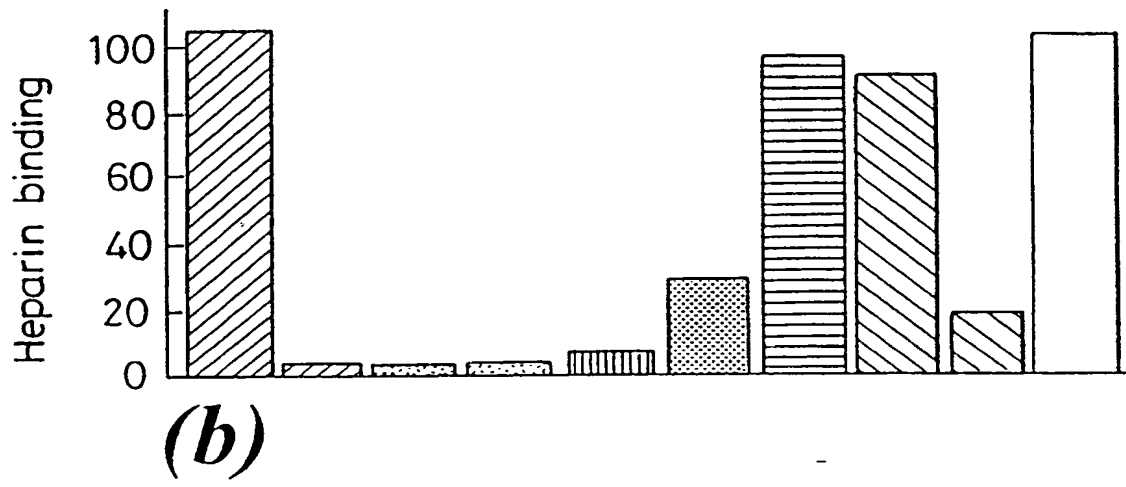
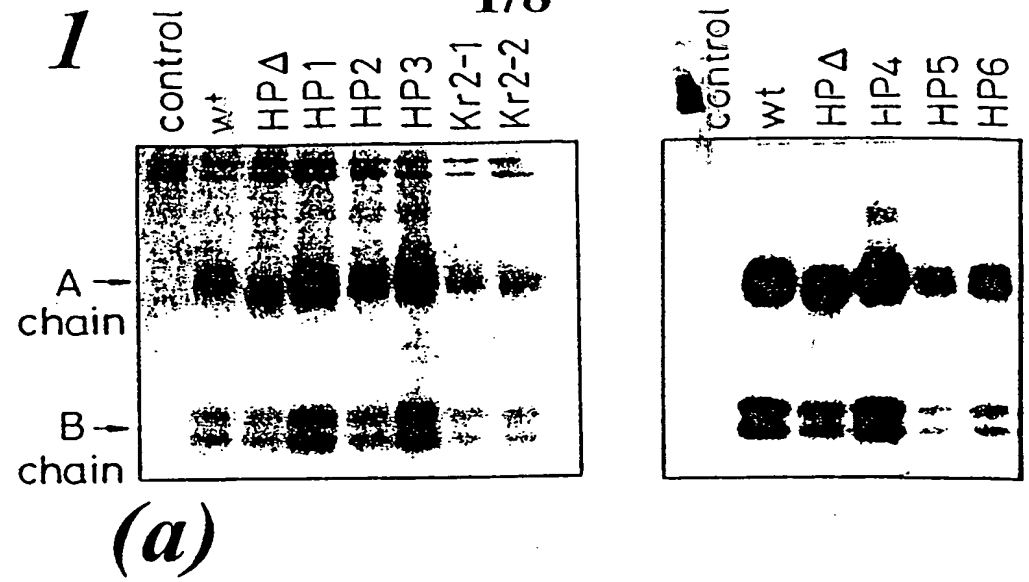
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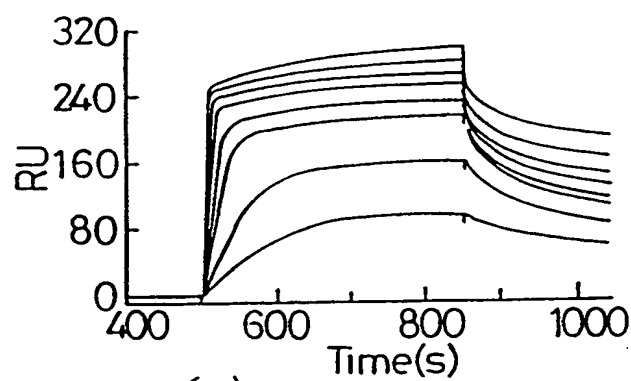
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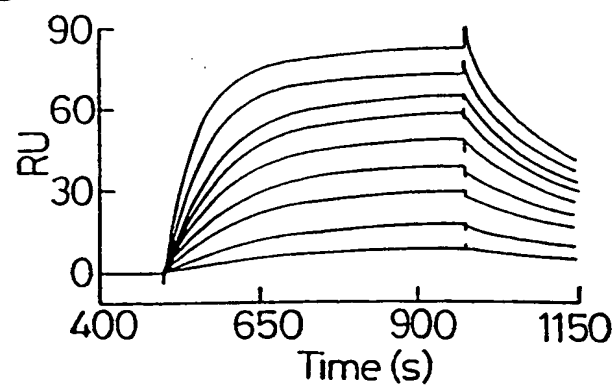
Fig 1 1/8



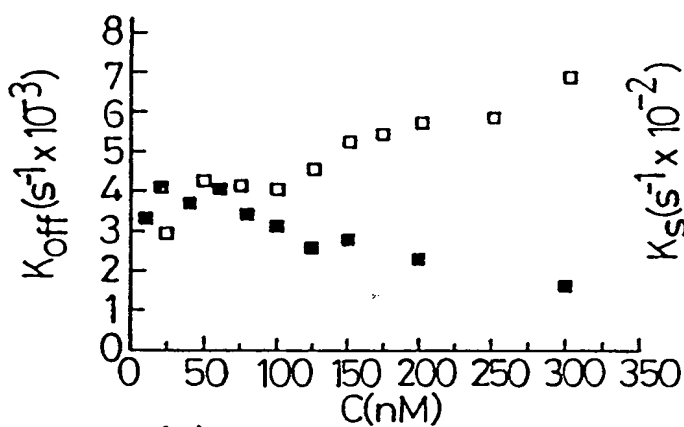
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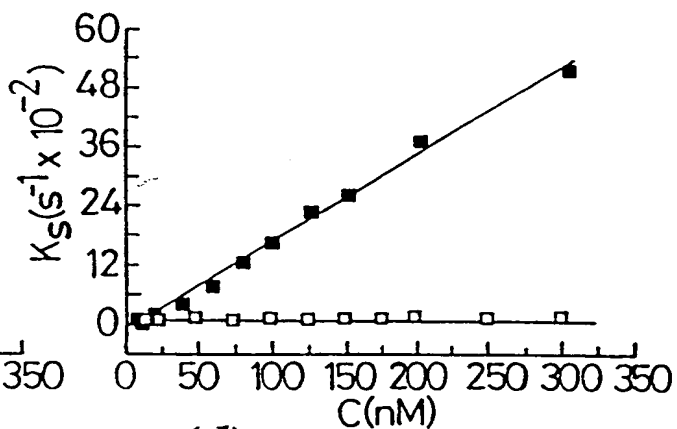
(a)



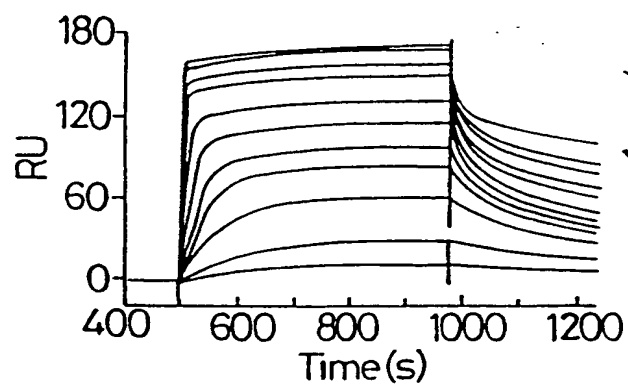
(b)



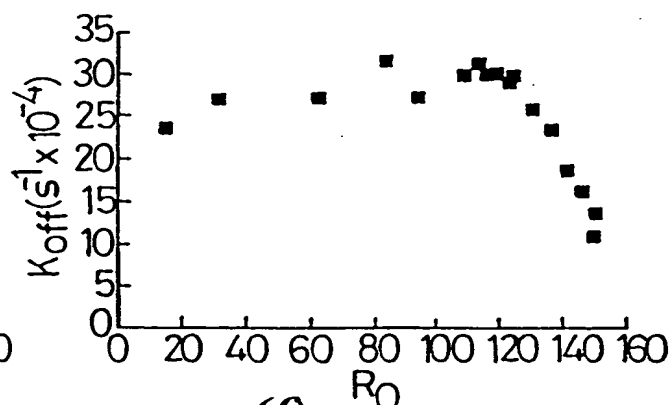
(c)



(d)



(e)



(f)

Fig. 2

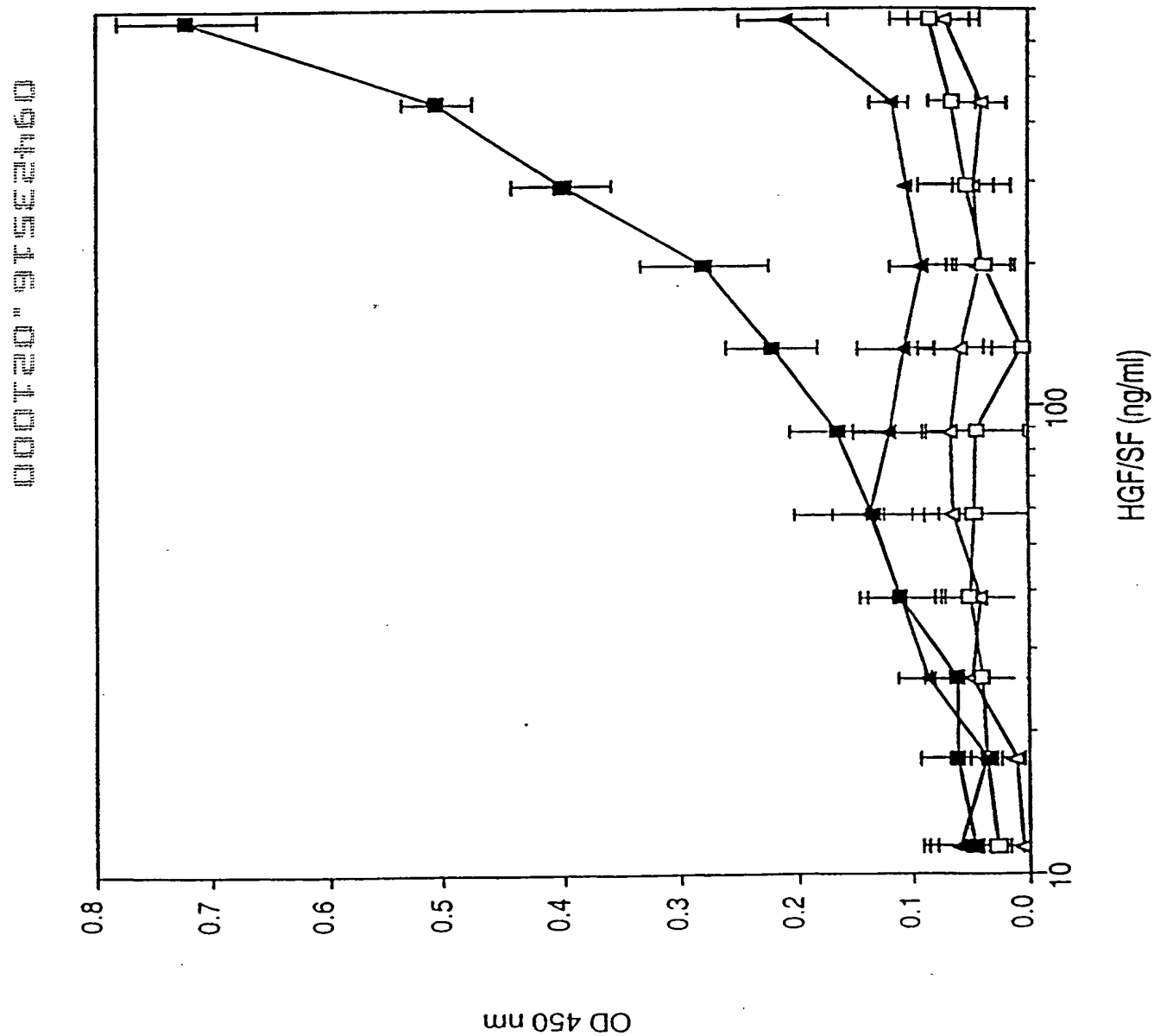
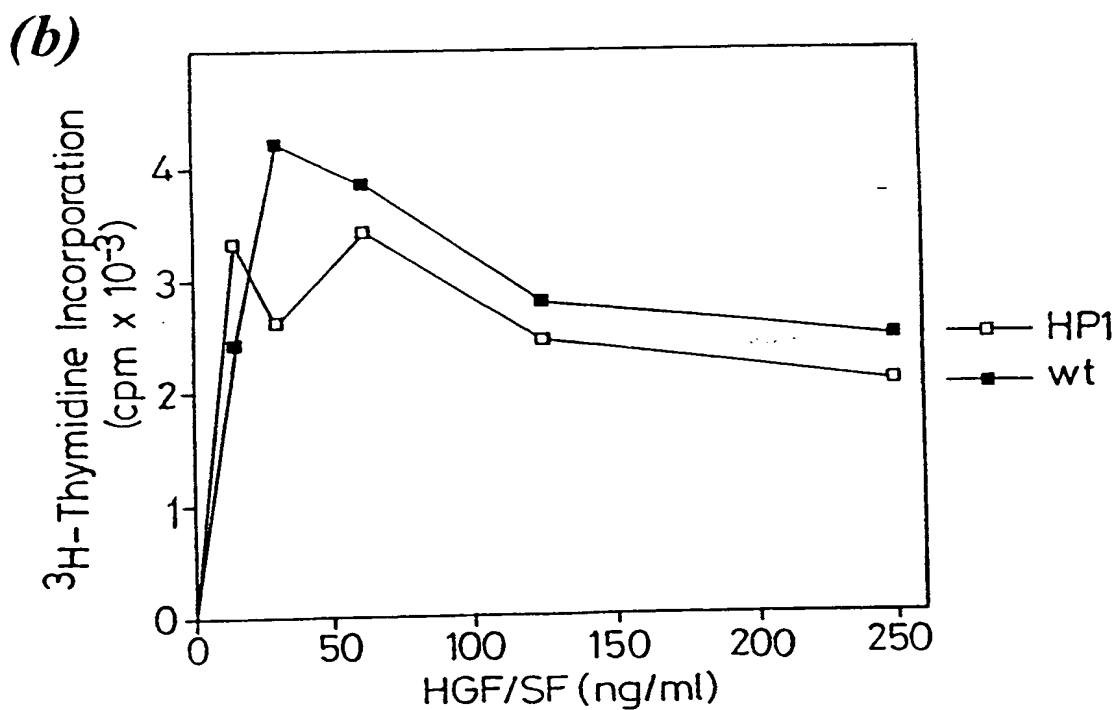
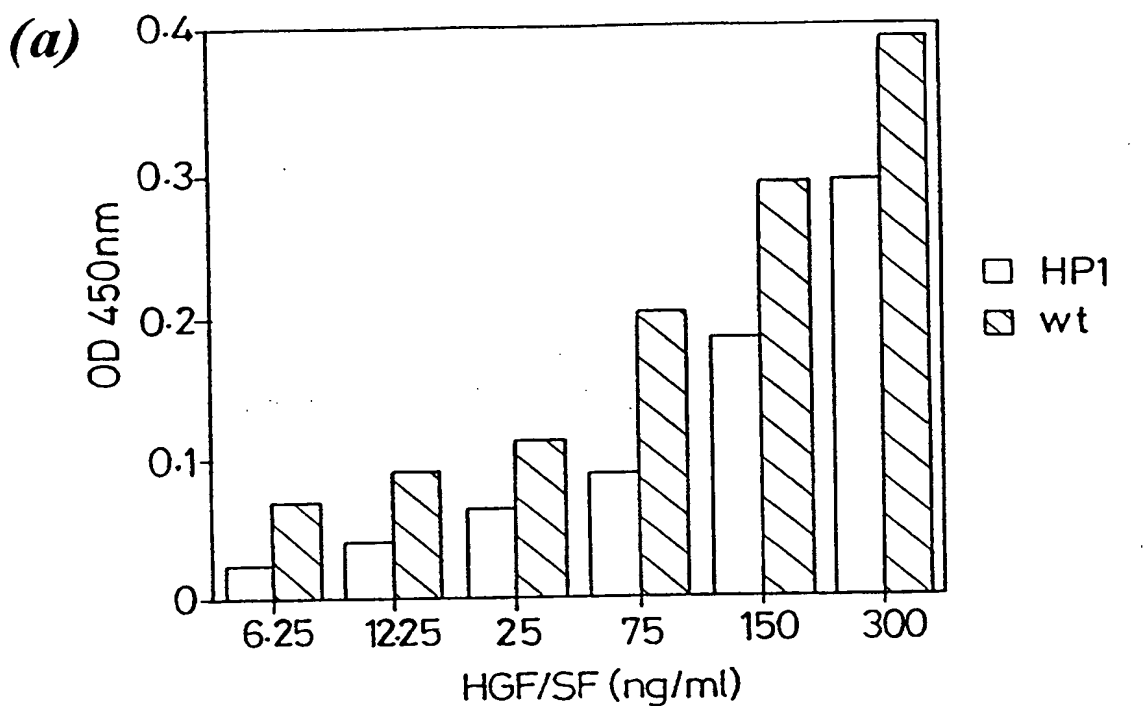


Fig. 3

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**Fig 4**

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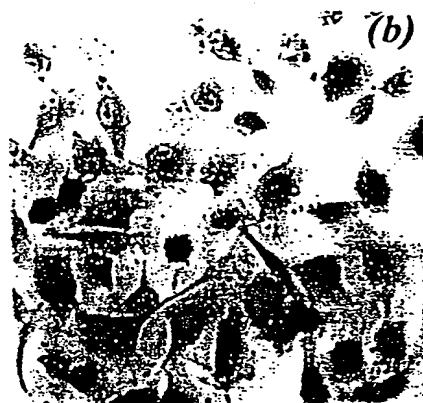


Fig. 5

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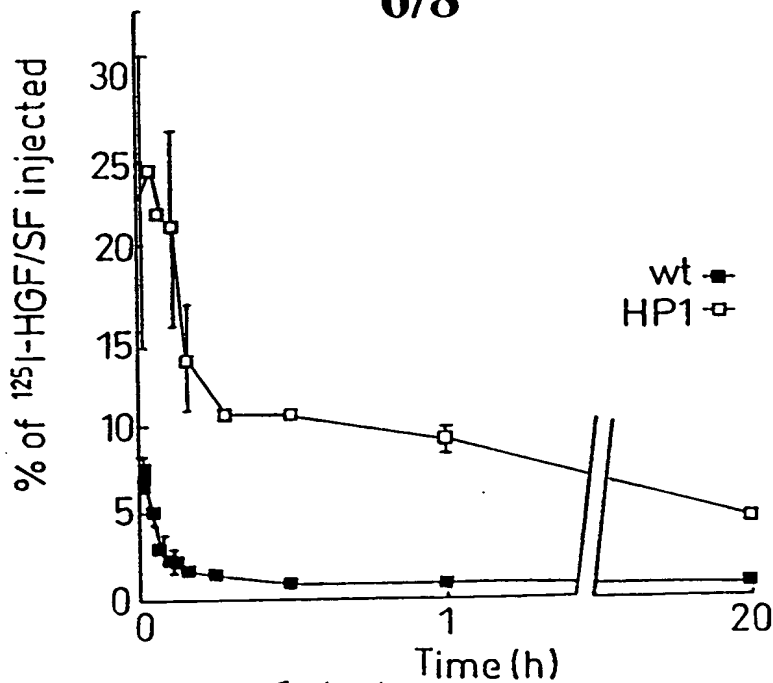


Fig. 6(a)

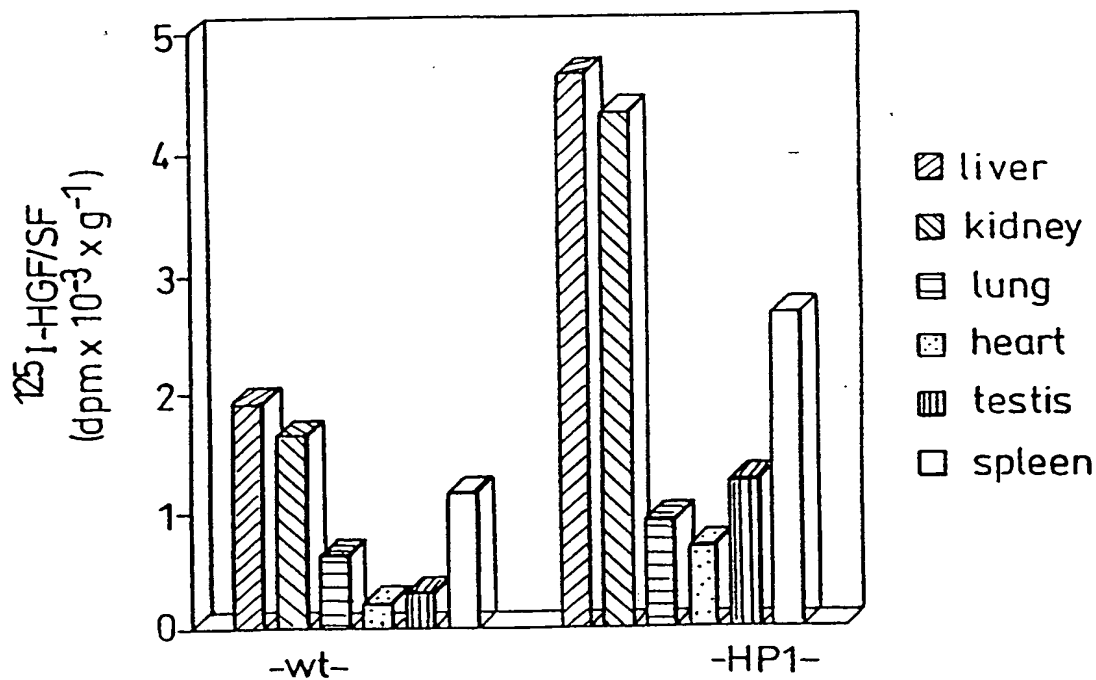
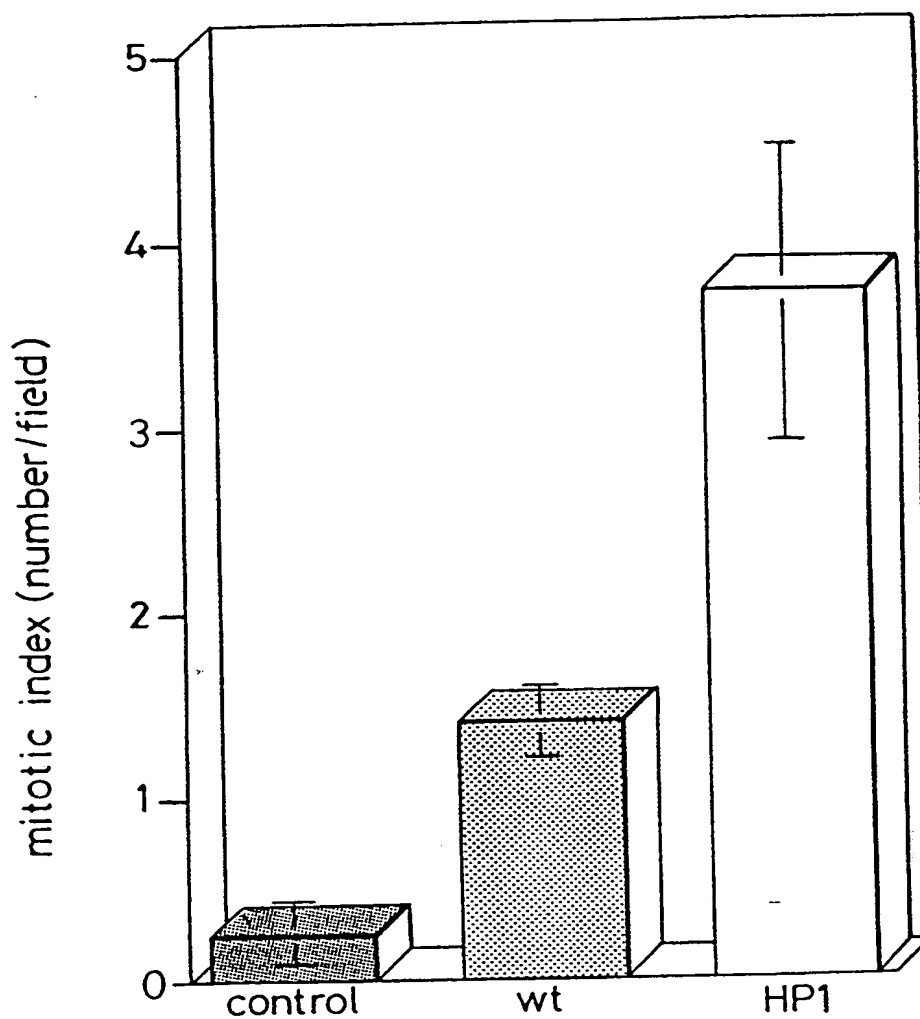


Fig 6(b)

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*Fig. 6(c)*

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HGF_HUMAN (sequence ex SwissProt)

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 70 80 90 100 110 120
 TKKVNTADQC ANRCTRNKGL PFTCKAFVFD KARKQCLWFP FNSMSSGVKK EFGHEFDLYE
 130 140 150 160 170 180
 NKDYIRNCII GKGRSYKGTV SITKSGIKCQ PWSSMIPHEH SFLPSSYRGK DLQENYCRNP
 190 200 210 220 230 240
 RGEEGGPWCF TSNPEVRYEV CDIPQCSEVE CMTCNESYR GLMDHTESGK ICQRWDHQTP
 250 260 270 280 290 300
 HRHKFLPERY PDKGFDDNYC RNPDGQPRPW CYTLDPHTRW EYCAIKTCAD NTMNDTDVPL
 310 320 330 340 350 360
 ETTECIQGQG EGYRGTVNTI WNGIPCQRWD SQYPHEHDMT PENFKCKDLR ENYCRNPDGS
 370 380 390 400 410 420
 ESPWCFTTDP NIRVGYSQI PNCDMSHGQD CYRGNGKNYM GNLSQTRSGL TCSMWDKNME
 430 440 450 460 470 480
 DLHRHIFWEP DASKLNENYC RNPDDDAHGP WCYTGNPLIP WDYCPISRCE GDTTPTIVNL
 490 500 510 520 530 540
 DHPVISCAT KQLRVVNGIP TRTNIGWMVS LRYRNKHICG GSLIKESWVL TARQCFPSRD
 550 560 570 580 590 600
 LKDYEAWLGI HDVHGRGDEK CKQVLNVSQ L VYGPEGSDLV LMKLARPAVL DDFVSTIDL P
 610 620 630 640 650 660
 NYGCTIPEKT SCSVYGWGYT GLINYDGLLR VAHLYIMGNE KCSQHHRGKV TLNESEICAG
 670 680 690 700 710 720
 AEKIGSGPCE GDYGGPLVCE QHKMRMVLGV IVPGRGCAIP NRPGIFVRVA YYAKWIHKII
 LTYKVPQS

Fig. 7